

# SCORE Search Results Details for Application 10568108 and Search Result 20070629\_130903\_us-10-568-108-2.rag.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10568108 and Search Result 20070629\_130903\_us-10-568-108-2.rag.

[Go Back to previous page](#)

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2007, 00:44:29 ; Search time 260 Seconds  
(without alignments)  
41.405 Million cell updates/sec

Title: US-10-568-108-2  
Perfect score: 109  
Sequence: 1 GAYDLRRRERQSRLRRRERQSR 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	109	100.0	22	9	ADY21199	Ady21199 Human cel
2	109	100.0	22	9	ADY21241	Ady21241 Gram-nega
3	109	100.0	22	9	ADY29688	Ady29688 Antibacte
4	109	100.0	23	9	ADY21209	Ady21209 Human cel
5	66	60.6	22	9	ADY21246	Ady21246 Gram-nega
6	66	60.6	22	9	ADY29693	Ady29693 Antibacte
7	66	60.6	197	1	AAP91931	Aap91931 Human hep
8	66	60.6	199	7	ADF17970	Adf17970 Human cat
9	66	60.6	199	7	ADG42089	Adg42089 Human cor
10	66	60.6	200	8	ABM84641	Abm84641 Human dia
11	66	60.6	221	2	AAR84663	Aar84663 Human hep
12	66	60.6	221	2	AAW04875	Aaw04875 Heparin b
13	66	60.6	222	2	AAR41935	Aar41935 Recombina
14	66	60.6	222	2	AAW73210	Aaw73210 CAP37 pro
15	66	60.6	222	7	ADG42088	Adg42088 Human pol
16	66	60.6	225	2	AAW88362	Aaw88362 Human mat
17	66	60.6	225	2	AAY21551	Aay21551 Human hep
18	66	60.6	225	2	AAW88118	Aaw88118 Mature hu
19	66	60.6	225	3	AAY71881	Aay71881 Human hep
20	66	60.6	225	3	AAY71882	Aay71882 Human hep
21	66	60.6	225	3	AAY71883	Aay71883 Human hep
22	66	60.6	225	3	AAY71876	Aay71876 Human mat
23	66	60.6	225	4	AAY71891	Aay71891 Human mat
24	66	60.6	225	7	ADE11587	Adel1587 Human mat
25	66	60.6	225	7	ADE11551	Adel1551 Human mat
26	66	60.6	225	8	ADK42019	Adk42019 Human hep
27	66	60.6	225	9	ADV21099	Adv21099 Human azu
28	66	60.6	225	9	ADX69310	Adx69310 Human hep
29	66	60.6	225	9	ADY82139	Ady82139 Human hep
30	66	60.6	225	10	AEJ02080	Aej02080 Human mat
31	66	60.6	226	2	AAR10669	Aar10669 Cationic
32	66	60.6	228	7	ADE11545	Adel1545 Human mat
33	66	60.6	232	2	AAW88364	Aaw88364 Human pro
34	66	60.6	232	2	AAY21550	Aay21550 Human hep
35	66	60.6	232	2	AAW88120	Aaw88120 Human hep
36	66	60.6	232	3	AAY71877	Aay71877 Human pre
37	66	60.6	232	10	AEJ02083	Aej02083 Human mat
38	66	60.6	238	7	ADE11549	Adel1549 Human mat
39	66	60.6	244	4	AAY71893	Aay71893 Human pre
40	66	60.6	245	7	ADE11547	Adel1547 Human mat
41	66	60.6	251	2	AAR10668	Aar10668 Cationic
42	66	60.6	251	2	AAR84666	Aar84666 Human hep
43	66	60.6	251	2	AAW88365	Aaw88365 Human pre
44	66	60.6	251	2	AAW88121	Aaw88121 Complete
45	66	60.6	251	3	AAY71878	Aay71878 Human pre

## ALIGNMENTS

## RESULT 1

ADY21199

ID ADY21199 standard; peptide; 22 AA.

XX

AC ADY21199;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human cell penetration vector peptide, DPV15b.

XX

KW cell permeabilization; virucide; antibacterial; cytostatic; vasotropic;

KW antimicrobial; antiapoptotic; antiangiogenic; pharmaceutical; cosmetics;

KW diagnostic; viral infection; metastasis; cell; vector.

XX

SCORE Search Results Details for Application 10568108  
and Search Result 20070629\_130905\_us-10-568-108-  
2.rup.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10568108 and Search Result 20070629\_130905\_us-10-568-108-2.rup.

Go Back to previous page

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2007, 00:47:37 ; Search time 343 Seconds  
(without alignments)  
68.766 Million cell updates/sec

Title: US-10-568-108-2  
Perfect score: 109  
Sequence: 1 GAYDLRRRERQSRLRRRERQSR 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	66	60.6	226	2	Q86SR2	HUMAN	Q86sr2 homo sapien
2	66	60.6	251	1	CAP7	HUMAN	P20160 homo sapien
3	61	56.0	1109	2	Q4BRC8	BURVI	Q4brc8 burkholderi
4	58	53.2	785	2	Q3JNU7	BURP1	Q3jnu7 burkholderi
5	57	52.3	386	2	Q29RC7	BRARE	Q29rc7 brachydanio
6	57	52.3	1117	2	Q7RHG1	PLAYO	Q7rhg1 plasmodium
7	55	50.5	336	2	Q1LJA3	RALME	Q1lja3 ralstonia m
8	54	49.5	77	1	PRT2	SEPOF	P80002 sepia offic

9	54	49.5	167	2	Q71RF1_HUMAN	Q71rf1 homo sapien
10	54	49.5	167	2	Q7Z780_HUMAN	Q7z780 homo sapien
11	54	49.5	194	2	Q9W1I6_DROME	Q9w1i6 drosophila
12	54	49.5	227	2	Q4RWW6_TETNG	Q4rww6 tetraodon n
13	54	49.5	237	2	Q98SE2_CHICK	Q98se2 gallus gall
14	54	49.5	238	1	U2AF1_MOUSE	Q9d883 mus musculu
15	54	49.5	239	1	U2AF1_HUMAN	Q01081 homo sapien
16	54	49.5	239	2	Q3KR55_RAT	Q3kr55 rattus norv
17	54	49.5	240	2	Q701P4_HUMAN	Q701p4 homo sapien
18	54	49.5	245	2	Q32NM8_XENLA	Q32nm8 xenopus lae
19	54	49.5	973	2	Q25VT3_MYCVN	Q25vt3 mycobacteri
20	54	49.5	1450	2	Q2H922_CHAGB	Q2h922 chaetomium
21	54	49.5	1867	2	Q19PP0_POPTR	Q19pp0 populus tri
22	54	49.5	1886	2	Q4SLF6_TETNG	Q4slf6 tetraodon n
23	53.5	49.1	176	2	Q5QMK8_ORYSA	Q5qmk8 oryza sativ
24	53	48.6	60	1	HSP1_MACAG	P42137 macropus ag
25	53	48.6	61	1	HSP1_MACEU	P42138 macropus eu
26	53	48.6	175	1	IF3_AQUAE	O67653 aquifex aeo
27	53	48.6	185	2	Q293G4_DROPS	Q293g4 drosophila
28	53	48.6	227	2	Q4SMD2_TETNG	Q4smd2 tetraodon n
29	53	48.6	249	2	Q8JHJ3_BRARE	Q8jhj3 brachydanio
30	53	48.6	250	2	Q4G0A1_BRARE	Q4g0a1 brachydanio
31	53	48.6	394	2	Q3JHD3_BURP1	Q3jhd3 burkholderi
32	53	48.6	550	2	Q2QXR6_ORYSA	Q2qxr6 oryza sativ
33	53	48.6	640	2	Q2S5C1_SALRD	Q2s5c1 salinibacte
34	53	48.6	957	1	PG03_MYCTU	P56877 mycobacteri
35	53	48.6	2002	2	Q2S5B6_SALRD	Q2s5b6 salinibacte
36	52.5	48.2	526	2	Q2KG03_MAGGR	Q2kg03 magnaporthe
37	52	47.7	63	1	HSP1_HYPMS	Q9glq1 hypsiprymno
38	52	47.7	118	2	Q7M4A3_LOLPE	Q7m4a3 loligo peal
39	52	47.7	175	2	Q5YPL2_NOCFA	Q5ypl2 nocardia fa
40	52	47.7	285	2	Q90626_CHICK	Q90626 gallus gall
41	52	47.7	286	2	Q84Q43_ORYSA	Q84q43 oryza sativ
42	52	47.7	292	1	SEN34_ASHGO	Q754t3 ashbya goss
43	52	47.7	298	2	Q292D3_DROPS	Q292d3 drosophila
44	52	47.7	311	2	Q6C9Y5_YARLI	Q6c9y5 yarrowia li
45	52	47.7	372	2	Q6DUB6_PIG	Q6dub6 sus scrofa

## ALIGNMENTS

## RESULT 1

## Q86SR2\_HUMAN

ID Q86SR2\_HUMAN PRELIMINARY; PRT; 226 AA.

AC Q86SR2;

DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2003, sequence version 1.

DT 13-JUN-2006, entry version 23.

DE AZU1 protein (Fragment).

GN Name=AZU1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

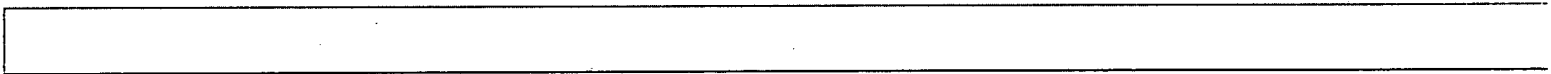
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,



[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10568108 and Search Result 20070629\_130907\_us-

GenCore version 6.2.1  
 Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2007, 00:49:00 ; Search time 34 Seconds  
 (without alignments)  
 62.258 Million cell updates/sec

Title: US-10-568-108-2  
 Perfect score: 109  
 Sequence: 1. GAYDLRRRERQSRLRRRERQSR 22

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	66	60.6	251	1	TRHUAZ	azurocidin precurs
2	54	49.5	77	2	B40973	spermatid-specific
3	54	49.5	240	2	A46179	U2 snRNP auxiliary
4	53	48.6	175	2	C70453	translation initia
5	53	48.6	957	2	D70835	hypothetical glyci
6	52	47.7	118	2	S56117	spermatid-specific
7	52	47.7	285	2	S53710	ribonucleoprotein
8	51	46.8	309	2	T41889	PE38 orf153 - Bomb
9	51	46.8	2019	2	T27702	hypothetical prote
10	49	45.0	43	2	D58213	protamine III - Am
11	49	45.0	261	2	AB3070	conserved hypothet

12	49	45.0	319	2	H98216	hypothetical prote
13	49	45.0	1407	1	S28589	trichohyalin - rab
14	48	44.0	36	2	JA0173	basic peptide - wi
15	48	44.0	234	2	S27956	arginine-rich prot
16	48	44.0	294	2	E87538	hypothetical prote
17	48	44.0	420	2	A45166	protein-lysine 6-o
18	48	44.0	517	1	A39038	l-caldesmon, nonmu
19	48	44.0	550	2	A46419	trophoblast-endoth
20	48	44.0	695	2	I54325	gene XE7 protein -
21	48	44.0	771	1	A33430	h-caldesmon - chic
22	47.5	43.6	694	2	T07638	SWH1 protein homol
23	47	43.1	27	1	SRAPC	protamine B - Russ
24	47	43.1	58	2	S10755	protamine St2b - h
25	47	43.1	62	2	S10754	protamine St2a - h
26	47	43.1	78	2	A40973	spermatid-specific
27	47	43.1	79	2	S56116	spermatid-specific
28	47	43.1	132	2	S10305	protamine - boll w
29	47	43.1	378	2	S04336	U1 snRNP 70K prote
30	47	43.1	406	2	T24492	hypothetical prote
31	47	43.1	531	2	A55887	caldesmon, non-mus
32	47	43.1	669	2	JC5662	hepatoma-derived g
33	47	43.1	728	2	T43632	serine/threonine p
34	47	43.1	792	2	T43630	serine/threonine p
35	47	43.1	793	1	JH0628	caldesmon - human
36	47	43.1	1075	2	T27623	hypothetical prote
37	47	43.1	1080	2	T27622	hypothetical prote
38	47	43.1	1549	1	A40691	trichohyalin - she
39	46.5	42.7	56	2	C58213	protamine II - Ame
40	46	42.2	126	2	S58321	probable membrane
41	46	42.2	224	2	F69444	conserved hypothet
42	46	42.2	321	1	A43681	immediate-early pr
43	46	42.2	321	2	C72869	hypothetical prote
44	46	42.2	354	2	T27099	hypothetical prote
45	46	42.2	580	1	S33743	aspartate-tRNA lig

## ALIGNMENTS

## RESULT 1

TRHUAZ

azurocidin precursor [validated] - human

N;Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neutrophil-derived C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C;Accession: A46268; A46455; S16450; S18520; S12881; S15445; S14738; B33913; A60708; B43600; A49211 R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992

A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte lineage are or

A;Reference number: A46268; MUID:92390417; PMID:1518849

A;Accession: A46268

A;Molecule type: DNA

A;Residues: 1-251 &lt;ZIM&gt;

A;Cross-references: UNIPROT:P20160; UNIPARC:UPI0000126ECD; GB:M96326; NID:g179301; PIDN:AAB59353.1;

A;Note: sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:112893, NCBIN:1128

R;Morgan, J.G.; Sukienicki, T.; Pereira, H.A.; Spitznagel, J.K.; Guerra, M.E.; Larrick, J.W.

J. Immunol. 147, 3210-3214, 1991

A;Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a microbicidal and c

A;Reference number: A46455; MUID:92013155; PMID:1919011

A;Accession: A46455

A;Molecule type: mRNA

A;Residues: 1-251 &lt;MOR&gt;

A;Cross-references: UNIPARC:UPI0000126ECD; GB:M96326; NID:g179301; PIDN:AAB59353.1; PID:g179302

A;Note: sequence extracted from NCBI backbone (NCBIN:60386, NCBI:60395)

R;Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabay, J.E.

SCORE Search Results Details for Application 10568108  
and Search Result 20070705\_094920\_us-10-568-108-  
1.rag.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10568108 and Search Result 20070705\_094920\_us-10-568-108-1.rag.

[Go Back to previous page](#)

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2007, 09:49:40 ; Search time 97 Seconds  
(without alignments)  
80.715 Million cell updates/sec

Title: US-10-568-108-1  
Perfect score: 76  
Sequence: 1' LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

- Database :
- A\_Geneseq\_200701:\*
    - 1: geneseqp1980s:\*
    - 2: geneseqp1990s:\*
    - 3: geneseqp2000s:\*
    - 4: geneseqp2001s:\*
    - 5: geneseqp2002s:\*
    - 6: geneseqp2003as:\*
    - 7: geneseqp2003bs:\*
    - 8: geneseqp2004s:\*
    - 9: geneseqp2005s:\*
    - 10: geneseqp2006s:\*
    - 11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			ID	Description
No.	Score	Match	Length	DB		

1	76	100.0	16	9	ADY21198	Ady21198	Human cel
2	76	100.0	16	9	ADY21240	Ady21240	Gram-nega
3	76	100.0	16	9	ADY29687	Ady29687	Antibacte
4	76	100.0	17	9	ADY21208	Ady21208	Human cel
5	65.5	86.2	17	4	AAG67730	Aag67730	Peptide H
6	65.5	86.2	17	6	ABP59497	Abp59497	Human hep
7	61.5	80.9	22	9	ADY21199	Ady21199	Human cel
8	61.5	80.9	22	9	ADY21241	Ady21241	Gram-nega
9	61.5	80.9	22	9	ADY29688	Ady29688	Antibacte
10	61.5	80.9	23	9	ADY21209	Ady21209	Human cel
11	52	68.4	476	4	ABB65935	Abb65935	Drosophil
12	51	67.1	541	2	AAW37148	Aaw37148	Mammalian
13	51	67.1	783	2	AAW37151	Aaw37151	Mouse neu
14	51	67.1	787	2	AAW37152	Aaw37152	Mouse neu
15	51	67.1	801	8	ADQ97686	Adq97686	Mouse can
16	51	67.1	802	2	AAW37153	Aaw37153	Mouse neu
17	51	67.1	802	4	AAU09139	Aau09139	Mammalian
18	50	65.8	390	3	AAB58287	Aab58287	Lung canc
19	50	65.8	467	7	ADM04921	Adm04921	Human pro
20	50	65.8	467	9	AEC87851	Aec87851	Human cDN
21	50	65.8	472	3	AAB23039	Aab23039	Human AVE
22	50	65.8	472	6	ADA23299	Ada23299	Human SEC
23	50	65.8	491	3	AAB23040	Aab23040	Human AVE
24	50	65.8	491	6	ADA23301	Ada23301	Human SEC
25	50	65.8	537	8	ADQ97689	Adq97689	Human can
26	50	65.8	570	9	AED84702	Aed84702	Ponsin in
27	50	65.8	719	8	ADQ97691	Adq97691	Human can
28	49	64.5	1898	2	AAY30795	Aay30795	A human t
29	49	64.5	1898	7	ADD48869	Add48869	Human Pro
30	49	64.5	1898	10	AEK65354	Aek65354	Human tri
31	48	63.2	70	9	AEC62684	Aec62684	PAP7 upst
32	48	63.2	97	3	AAB43257	Aab43257	Human ORF
33	48	63.2	126	8	ADY22957	Ady22957	Plant ful
34	48	63.2	319	6	ABU70389	Abu70389	Human adi
35	48	63.2	364	8	ADS34465	Ads34465	POSH prot
36	48	63.2	364	8	ADU69062	Adu69062	Human GOC
37	48	63.2	528	4	AAM78918	Aam78918	Human pro
38	48	63.2	528	8	ADS34467	Ads34467	POSH prot
39	48	63.2	528	8	ADS34466	Ads34466	POSH prot
40	48	63.2	528	8	ADS34464	Ads34464	POSH prot
41	48	63.2	528	8	ADU69063	Adu69063	Human GOC
42	48	63.2	528	8	ADU69061	Adu69061	Human GOC
43	48	63.2	528	8	ADU69064	Adu69064	Human GOC
44	48	63.2	528	9	ADX06778	Adx06778	Cyclin-de
45	48	63.2	545	4	AAM79902	Aam79902	Human pro
46	47	61.8	239	4	ABG16782	Abg16782	Novel hum
47	47	61.8	247	8	ADX90684	Adx90684	Plant ful
48	47	61.8	247	8	ADX90698	Adx90698	Plant ful
49	47	61.8	311	3	AAB42307	Aab42307	Human ORF
50	47	61.8	658	4	ABB65632	Abb65632	Drosophil

## ALIGNMENTS

## RESULT 1

ADY21198

ID ADY21198 standard; peptide; 16 AA.

XX

AC ADY21198;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human cell penetration vector peptide, DPV15.



# SCORE Search Results Details for Application 10568108 and Search Result 20070705\_094922\_us-10-568-108-1.rup.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10568108 and Search Result 20070705\_094922\_us-10-568-108-1.rup.

[Go Back to previous page](#)

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2007, 09:49:44 ; Search time 353 Seconds  
(without alignments)  
48.595 Million cell updates/sec

Title: US-10-568-108-1  
Perfect score: 76  
Sequence: 1 LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	52	68.4	2753	2 Q3KN34_DROME	Q3kn34 drosophila
2	52	68.4	2935	2 Q7Z1Y4_DROME	Q7z1y4 drosophila
3	52	68.4	2946	2 Q9W053_DROME	Q9w053 drosophila
4	51	67.1	513	2 Q9DEG2_CHICK	Q9deg2 gallus gall
5	51	67.1	526	2 Q5XHX3_RAT	Q5xhx3 rattus norv
6	51	67.1	550	2 O93263_CHICK	O93263 gallus gall
7	51	67.1	784	2 Q90YB5_CHICK	Q90yb5 gallus gall
8	51	67.1	802	1 ENAH_MOUSE	Q03173 mus musculu

9	50	65.8	320	2	Q4DK01_TRYCR	Q4dk01 trypanosoma
10	50	65.8	391	2	Q4CTG4_TRYCR	Q4ctg4 trypanosoma
11	50	65.8	591	1	ENAH_HUMAN	Q8n8s7 homo sapien
12	49	64.5	359	2	Q16LV4_AEDAE	Q16lv4 aedes aegyp
13	49	64.5	1190	2	Q519A0_ENTHI	Q519a0 entamoeba h
14	49	64.5	1439	2	Q5CQG9_CRYPV	Q5cqg9 cryptospori
15	49	64.5	1898	1	TRHY_HUMAN	Q07283 homo sapien
16	49	64.5	1943	2	Q5VUI3_HUMAN	Q5vui3 homo sapien
17	48	63.2	260	2	Q5ZD80_ORYSA	Q5zd80 oryza sativ
18	48	63.2	372	2	Q6DUB6_PIG	Q6dub6 sus scrofa
19	48	63.2	523	2	Q5RHP5_BRARE	Q5rhp5 brachydanio
20	48	63.2	527	1	GCP60_HUMAN	Q9h3p7 h golgi res
21	48	63.2	540	2	Q2J1R0_RHOP2	Q2j1r0 rhodopseudo
22	48	63.2	668	2	Q57VZ5_9TRYP	Q57vz5 trypanosoma
23	48	63.2	685	1	CS021_PONPY	Q5rbh3 pongo pygma
24	48	63.2	1094	2	Q26774_9TRYP	Q26774 trypanosoma
25	48	63.2	1784	2	Q54TU2_DICDI	Q54tu2 dictyosteli
26	48	63.2	1914	2	Q3GJD8_CHLPH	Q3gjd8 prosthecoch
27	47	61.8	154	2	Q6YTG1_ORYSA	Q6ytg1 oryza sativ
28	47	61.8	359	2	Q5Z6A2_ORYSA	Q5z6a2 oryza sativ
29	47	61.8	524	1	GCP60_MOUSE	Q8bmp6 m golgi res
30	47	61.8	544	2	Q5B8X7_EMENI	Q5b8x7 emericella
31	47	61.8	545	2	Q4CVF8_TRYCR	Q4cvf8 trypanosoma
32	47	61.8	545	2	Q4CMJ9_TRYCR	Q4cmj9 trypanosoma
33	47	61.8	791	2	Q26LI9_XANP2	Q26li9 xanthobacte
34	47	61.8	800	2	Q9Y102_DROME	Q9y102 drosophila
35	47	61.8	925	2	Q2QNZ9_ORYSA	Q2qnz9 oryza sativ
36	47	61.8	971	2	Q6C1S3_YARLI	Q6c1s3 yarrowia li
37	47	61.8	1046	2	Q3JNP6_BURP1	Q3jnp6 burkholderi
38	47	61.8	1229	2	Q6C1W6_YARLI	Q6c1w6 yarrowia li
39	47	61.8	2486	2	Q9VXM5_DROME	Q9vxm5 drosophila
40	46	60.5	117	2	Q9VNS4_DROME	Q9vns4 drosophila
41	46	60.5	129	2	Q9VNS6_DROME	Q9vns6 drosophila
42	46	60.5	289	1	CWC23_SCHPO	Q9p7c6 schizosacch
43	46	60.5	298	2	Q1LZ42_DROME	Q1lz42 drosophila
44	46	60.5	399	2	Q510K9_ENTHI	Q510k9 entamoeba h
45	46	60.5	436	2	Q624C9_CAEBR	Q624c9 caenorhabdi
46	46	60.5	536	2	Q50N21_ENTHI	Q50n21 entamoeba h
47	46	60.5	537	2	Q9U3Z8_ENTHI	Q9u3z8 entamoeba h
48	46	60.5	564	2	Q4SFM4_TETNG	Q4sfm4 tetraodon n
49	46	60.5	586	2	Q34WM2_9GAMM	Q34wm2 alkalilimni
50	46	60.5	589	2	Q1EA13_COCIM	Q1ea13 coccidioide

## ALIGNMENTS

## RESULT 1

Q3KN34\_DROME

ID Q3KN34\_DROME PRELIMINARY; PRT; 2753 AA.

AC Q3KN34;

DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.

DT 08-NOV-2005, sequence version 1.

DT 18-APR-2006, entry version 5.

DE GH18167p (Fragment).

GN Name=CG33484-RA;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1].

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Berkeley;

RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10568108 and Search Result 20070705\_094924\_us-

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2007, 09:50:55 ; Search time 31 Seconds  
(without alignments)  
49.660 Million cell updates/sec

Title: US-10-568-108-1  
Perfect score: 76  
Sequence: 1 LRRERQSRLRRERQSR 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	49	64.5	1898	1	A45973	trichohyalin - hum
2	48	63.2	1094	2	A53435	vesicular transpor
3	46	60.5	675	2	D83405	conserved hypothet
4	46	60.5	699	2	E84565	hypothetical prote
5	45	59.2	1027	2	T46481	hypothetical prote
6	45	59.2	1233	2	T30989	serine/threonine p
7	45	59.2	3498	2	T22330	hypothetical prote
8	44	57.9	36	2	JA0173	basic peptide - wi
9	44	57.9	263	2	B84778	hypothetical prote
10	44	57.9	454	2	T19433	hypothetical prote
11	44	57.9	679	2	T00636	hypothetical prote

12	44	57.9	1407	1	S28589	trichohyalin - rab
13	43	56.6	118	2	S56117	spermatid-specific
14	43	56.6	308	2	F95416	hypothetical prote
15	43	56.6	413	2	H88481	protein let-756 [i
16	43	56.6	427	2	AE2512	hypothetical prote
17	43	56.6	444	2	T32648	hypothetical prote
18	43	56.6	468	1	FOMVMU	gag polyprotein -
19	43	56.6	538	1	FOMVM	gag polyprotein -
20	43	56.6	569	2	T43531	probable potassium
21	43	56.6	733	2	G84668	hypothetical prote
22	43	56.6	1175	2	T22491	hypothetical prote
23	42	55.3	58	2	S34045	protamine - North
24	42	55.3	78	2	A40973	spermatid-specific
25	42	55.3	79	2	S56116	spermatid-specific
26	42	55.3	99	2	B46598	ski-related protei
27	42	55.3	126	2	S58321	probable membrane
28	42	55.3	296	2	S73007	hypothetical prote
29	42	55.3	513	2	T03916	hypothetical prote
30	42	55.3	614	2	AB2304	two-component hybr
31	42	55.3	684	1	TVHUSN	transforming prote
32	42	55.3	690	2	I51298	transforming prote
33	42	55.3	704	2	T24517	hypothetical prote
34	42	55.3	710	2	AE1956	hypothetical prote
35	42	55.3	737	2	T15597	hypothetical prote
36	42	55.3	749	2	T08101	outer dynein arm d
37	42	55.3	788	2	G89901	hypothetical prote
38	42	55.3	810	2	T44430	protein PV100 [imp
39	42	55.3	919	2	F81998	ribonuclease E (EC
40	42	55.3	919	2	F81225	ribonuclease E NMB
41	42	55.3	1017	2	T15598	hypothetical prote
42	42	55.3	1131	2	S22266	FUN30 protein - ye
43	42	55.3	2550	2	B53435	vesicular transpor
44	41	53.9	45	2	B58208	protamine II-1 - p
45	41	53.9	47	2	F58208	protamine II-5 - p
46	41	53.9	47	2	E58208	protamine II-4 - p
47	41	53.9	142	2	B72667	hypothetical prote
48	41	53.9	227	2	T46264	hypothetical prote
49	41	53.9	279	2	T26166	hypothetical prote
50	41	53.9	325	2	H96815	hypothetical prote

ALIGNMENTS

RESULT 1  
A45973  
trichohyalin - human  
C;Species: Homo sapiens (man)  
C;Date: 03-May-1994 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C;Accession: A45973  
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, P.M.  
J. Biol. Chem. 268, 12164-12176, 1993  
A;Title: The structure of human trichohyalin. Potential multiple roles as a functional EF-hand-like  
A;Reference number: A45973; MUID:93280194; PMID:7685034  
A;Accession: A45973  
A;Molecule type: DNA  
A;Residues: 1-1898 <LEE>  
A;Cross-references: UNIPROT:Q07283; UNIPARC:UPI000013738B; GB:L09190; NID:g292835; PIDN:AAA65582.1;  
A;Note: authors translated the codon AGG for residue 1714 as Pro  
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sheath cells  
C;Genetics:  
A;Gene: GDB:THH  
A;Cross-references: GDB:136223; OMIM:190370  
A;Map position: 1q21-1q21  
C;Superfamily: trichohyalin; calmodulin repeat homology

2

CN GenBank CA04087  
 CN GenBank CA04087 (translated from: GenBank CT005261)  
 SOL 1219  
 LC STN Files: CA, CAPLUS

SEQ 501 FVPSMPSIP HFLRTFIAPD VENVYWTETQ AACILYNPFK RYKAIRRRAR  
 =====  
 551 FVRDKRMKLP RVYQLEHRE VLLTRLDAGK EDVAAAEENT PGYVVTQFA  
 ==

HITS AT: 540-553

L10 ANSWER 8 OF 11 REGISTRY COPYRIGHT 2007 ACS on STN  
 RN 661663-02-1 REGISTRY  
 CN Protein (corn clone 700452394\_Flt.pep fragment) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN 942: PN: US20040034868 SEQID: 44942 claimed protein  
 SOL 176  
 LC STN Files: CA, CAPLUS

SEQ 101 WRLSLVGLW RRPRLVRLR RPLVLPWML RLMSDHRPL RLIIAGGD  
 =====

HITS AT: 111-126

L10 ANSWER 9 OF 11 REGISTRY COPYRIGHT 2007 ACS on STN  
 RN 610323-99-4 REGISTRY  
 CN L-Alanine, L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl- (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN 49: PN: US20030190364 SEQID: 48 claimed protein  
 SOL 28  
 LC STN Files: CA, CAPLUS, USPATFULL

SEQ 1 FHRRKAFHR RIKAFHRIK AFHRRKKA  
 =====

HITS AT: 2-23

L10 ANSWER 10 OF 11 REGISTRY COPYRIGHT 2007 ACS on STN  
 RN 610317-86-7 REGISTRY  
 CN L-Alanine, L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl- (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN 26: PN: US20030190364 SEQID: 25 claimed sequence  
 SOL 21  
 LC STN Files: CA, CAPLUS, USPATFULL

SEQ 1 FHRRKAFHR RIKAFHRIK A  
 =====

HITS AT: 2-16

L10 ANSWER 11 OF 11 REGISTRY COPYRIGHT 2007 ACS on STN  
 RN 610317-84-5 REGISTRY  
 CN L-Alanine, L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl-L-alanyl-L-phenylalanyl-L-histidyl-L-arginyl-L-arginyl-L-isoleucyl-L-  
 lysyl- (9CI) (CA INDEX NAME)

3

OTHER NAMES:  
 CN 24: PN: US20030190364 SEQID: 23 claimed sequence  
 SOL 21  
 LC STN Files: CA, CAPLUS, USPATFULL

SEQ 1 FHRRKAFHR RIKAFHRIK A  
 =====

HITS AT: 2-16

=> file zcaplus  
 FILE 'ZCAPLUS' ENTERED AT 14:56:19 ON 03 JUL 2007  
 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
 COPYRIGHT (C) 2007 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS is strictly prohibited.

FILE COVERS 1907 - 3 JUL 2007 VOL 147 ISS 2  
 FILE LAST UPDATED: 2 JUL 2007 (20070702/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.  
 'OBI' IS DEFAULT SEARCH FIELD FOR 'ZCAPLUS' FILE

=> d l13 tot 1b1b abs

L13 ANSWER 1 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
 ACCESSION NUMBER: 2005:161031 ZCAPLUS Full-Text  
 DOCUMENT NUMBER: 142:266763  
 TITLE: peptide vectors facilitating intracellular or intranuclear delivery of drugs and their therapeutic use  
 INVENTOR(S): Avramess, Alexandre  
 PATENT ASSIGNEE(S): Diacos, Fr.  
 SOURCE: PCT Int. Appl., 102 pp.  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 3  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005016960	A2	20050224	WO 2004-1B2936	20040813
WO 2005016960	A3	20050407		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GR, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,				

4

BR 2836712	AI	200503962	EP 2003-97962	20030814
EP 1512696	AI	200503019	EP 2003-292030	20030814
R: AT, BE, CH, DE, DK, ES, FR, GB, GE, IT, LI, LU, NL, SE, MC, PT				
IE, SI, IT, LV, FI, RO, MK, TR, BI, CZ, EN, HU, SK				
AU 2004265159	AI	200503024	AU 2004-265159	20040813
CA 2536670	AI	200502024	CA 2004-2536670	20040813
EP 1654285	A2	200605010	EP 2004-769334	20040813
R: AT, BE, CH, DE, DK, ES, FR, GB, GE, IT, LI, LU, NL, SE, MC, PT				
IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK				
BR 2004013561	A	2006101010	BR 2004-135621	20060813
US 20070642492	AI	200702222	US 2006-568108	20060213
PRIORITY APPL. INFO:			EP 2003-292030	A 20030814

L13 ANSWER 2 OF 11  
ZCAPLUS COPYRIGHT 2007 ACS on STEM  
ACCESSION NUMBER: 1989-110599 ZCAPLUS Full-text  
DOCUMENT NUMBER: 130-192714  
TITLE: Peptides derived from antibodies to DNA for targeting  
of substances to cells and stimulation of uptake  
INVENTOR(S): Ternynck, Therese; Avrameas, Alexander;

EVENT NO.	KIND	DATE	APPLICATION NO.	DATE
93907414	A1	19390218	MO 1998-FR1740	19980804
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, C, C, DE				
DK, EE, ES, FI, GB, GE, GM, HR, HU, ID, IL, IS, JP, KE, KG, KR				
KP, KR, KZ, LK, LR, LS, LT, LV, LM, MD, MG, MK, MN, MM, MX				
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT				
UA, UG, US, UZ, VN, YU, ZW				
RM: GH, GM, GE, GR, IS, KM, SD, SE, UG, ZW, AT, BE, CH, CY, DE, DK, ES				
FI, FR, GB, GS, LR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI				

**AB** Peptides derived from antibodies to DNA that can penetrate cell membranes and

L13 ANSWER 3 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
 ACCESSION NUMBER: 1998-789501 ZCAPLUS [Full-text](#)  
 DOCUMENT NUMBER: 130:149222  
 TITLE: Efficient Gene Delivery by a Peptide Derived from a  
 Monoclonal anti-DNA Antibody  
 AUTHOR(S): Avramatz, Alexandre; Tenynck, Therese;  
 Gami, Leila; Buttin, Gerard  
 CORPORATE SOURCE: Unite de Genetique Somatique (URA CNRS 1960) and Un

We recently reported that translocating murine polyclonal anti-DNA antibodies can be used as vectors for the transfer of macromols. into cells growing in culture. We show here that two such monoclonal antibodies (420.8 and F4.1) conjugated to polylysine with a high (93) but not a low (19) number of lysine residues can transfer genes in the presence of serum. A 30 amino acid long peptide, VALIRGVSTYTSIDVWAGRTQKNNRA (peptide p3), corresponding to joined heavy-chain complementary-determining regions 2 and 3 of F4.1 antibody and carrying 19 lysine residues at its N-terminal, was found to be an efficient vector for the transfection of the luciferase gene into 3T3 and CCL39 cells in the presence of serum. Addition of 0.23 M glycerol during transfection considerably enhanced gene delivery. These results show that

conjugation of a short polylysine tail converted a spontaneously internalizing peptide into a potent non-toxic plasmid vector.

REFERENCE COUNT: 39  
THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 4 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 1998:311775 ZCAPLUS Full-text  
DOCUMENT NUMBER: 129:80389  
TITLE: Polyreactive anti-DNA monoclonal antibodies and a derived peptide as vectors for the intracytoplasmic and intranuclear translocation of macromolecules

AUTHOR(S): Avrameas, Alexandre; Ternynck, Therese; Nato, Faridabano; Buttin, Gerard; Avrameas, Stratis  
CORPORATE SOURCE: Unite de Genetique Somaque, Departement de Biotechnologie, Institut Pasteur, Paris, 75015, Fr.  
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(10), 5601-5606  
CODEN: PNASAF, ISSN: 0027-8424

PUBLISHER: National Academy of Sciences  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Naturally occurring polyreactive anti-DNA mAbs derived from a nonimmunized (NZB + NZW) F1 mouse with spontaneous lupus erythematosus penetrated and accumulated in the nuclei of a variety of cultured cells. These mAbs and their F(ab')<sub>2</sub> and Fab' fragments, covalently coupled to fluorescein, peroxidase, or a 15-mer polynucleotide, also translocated to the cell nuclei. A 30-amino acid peptide corresponding to the combined sequences of the complementary-determining regions 2 and 3 of the heavy chain variable region of one mAb was able to penetrate into the cytoplasm and nucleus of cells of several lines. This peptide recognized DNA and was strongly polyreactive. Streptavidin-peroxidase conjugates complexed with the N-biotinylated peptide were rapidly translocated into cells. Similarly, peroxidase or anti-peroxidase polyclonal antibodies covalently coupled to the N-cysteinylation peptide through an heterobifunctional maleimide cross-linker were also rapidly internalized and frequently accumulated in nuclei. The peptide carrying 19 lysine residues at its N-terminal was highly effective in transfecting 3T3 cells with a plasmid containing the luciferase gene. Thus, penetrating mAbs and derived peptides are versatile vectors for the intracellular delivery of proteins and genes.

REFERENCE COUNT: 30  
THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 5 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 1997:313328 ZCAPLUS Full-text  
DOCUMENT NUMBER: 127:134458  
TITLE: Mimotopes of polyreactive anti-DNA antibodies identified using phage-display peptide libraries

AUTHOR(S): Sibille, Pierre; Ternynck, Therese; Nato, Faridabano; Buttin, Gerard; Strosberg, Donny; Avrameas, Alexandre  
CORPORATE SOURCE: Institut Cochin Genetique Moleculaire, Paris, Fr.  
SOURCE: European Journal of Immunology (1997), 27(5), 1221-1228  
CODEN: EJIMAF, ISSN: 0014-2980

PUBLISHER: VCH  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB Three monoclonal IgG2a anti-DNA polyreactive autoantibodies, derived from lupus-prone mice (NZB + NZW)F1, were studied by surface plasmon resonance (Biacore) anal. using 3 different synthetic double-stranded (ds)

oligonucleotides of 25, 30, and 25 base pairs (bp). These monoclonal antibodies (mAb) exhibited dissociation rate constants (K<sub>off</sub>) ranging from 0.0001 (mAb F14.6 and F4.1) to 0.01/s (mAb J20.8) and K<sub>on</sub> ranging from 2.1-105 to 2.106 /M/s. The screening of a constrained random peptide library displayed on M13 bacteriophages on these mAb allowed the determination of the specific consensus motifs (mimotopes) for mAb F14.6 and J20.8, but not for mAb F4.1. No cross-reaction was observed between F14.6- and J20.8-specific peptides (and vice versa). Binding of all phages selected on F14.6 was inhibited with 700 ng/mL soluble DNA. The binding of a group of peptides selected on J20.8 was inhibited by 400 ng/mL soluble DNA, of a 2nd group by 2500 ng/mL, while binding of a 3rd group was not inhibited. The determined consensus sequences do not match with known sequences. Peptides specific for F14.6 share neg. charges and aromatic rings that may mimic a DNA backbone, while peptides selected with J20.8 do not bear any neg. charge, implying a different kind of mol. recognition, for example hydrogen or salt bonds. The peptides selected on J20.8 also bind serum antibodies from human patients with systemic lupus erythematosus. BALB/c mice immunized with some of the selected phages exhibit high serum titers of IgG3 anti-dsDNA antibodies, further supporting the hypothesis that peptide epitopes may mimic an oligonucleotide structure.

L13 ANSWER 6 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 1996:181560 ZCAPLUS Full-text  
DOCUMENT NUMBER: 124:230006  
TITLE: Peptide fragment specific for feline immunodeficiency virus (FIV) and its use as a diagnostic reagent for antibody detection and disease diagnosis

INVENTOR(S): Avrameas, Alexandre; Panchino, Gianfranco; Sibille, Pierre; Sonigo, Pierre; Strosberg, Arthur Donny  
PATENT ASSIGNEE(S): Centre National de la Recherche Scientifique (CNRS), Fr.

SOURCE: Eur. Pat. Appl., 12 pp.  
DOCUMENT TYPE: CODEN: EPXNDM  
LANGUAGE: Patent  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 688790	A1	19951227	EP 1995-40116	19950607
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
FR 2721031	A1	19951215	FR 1994-7062	19940609
FR 2721031	B1	19960726		
US 5648209	A	19970715	US 1995-487485	19950607
PRIORITY APPL. INFO:				
AB A peptide fragment P253 was prepared from the Env protein of feline immunodeficiency virus Mo strain, derived from positions 693-709 of the protein, wherein the 3rd and/or 10th residues are replaced with cysteine or serine. The peptide is used to detect antibodies to the virus in biol. fluids as a diagnostic kit. The peptide proved more sensitive in a comparative ELISA than did P237.				

L13 ANSWER 7 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 1996:115032 ZCAPLUS Full-text  
DOCUMENT NUMBER: 124:143569  
TITLE: Expression of a mannose/fucose membrane lectin on



**AUTHOR(S):** human dendritic cells  
Avrameas, Alexandre; McIlroy, Dorian;  
Hosmalin, Anne; Autran, Brigitte; Debre, Patrice;  
Monsigny, Michel; Roche, Annie Claude; Midoux, Patrick  
**CORPORATE SOURCE:** Glycobiol., Cent Biophysique Molculaire, CNRS, Univ.  
d'Orleans, Orleans, Fr.

**SOURCE:** European Journal of Immunology (1996), 26(2), 394-400  
CODEN: EJIMAF; ISSN: 0014-2980

**PUBLISHER:** VCH

**DOCUMENT TYPE:** Journal

**LANGUAGE:** English

**AB** Dendritic cells (DC) are the most efficient antigen presenting cells for T lymphocytes. CD1a+ CD14- DC with high antigen-presenting capacities can now be obtained easily from adherent peripheral blood monocytes by culture in the presence of granulocyte/macrophage colony-stimulating factor and interleukin-4 (Sallusto et al., 1994). Human macrophages express a membrane lectin, or sugar-specific receptor, which specifically mediates the binding and endocytosis of mannose- and fucose-terminated glycoproteins and is involved in the phagocytosis of pathogens. A similar lectin activity was sought on cultured human DC using flow cytometry and confocal microscopy to detect binding and internalization of fluoresceinated neoglycoproteins [bovine serum albumin (BSA) substituted with sugar residues]. Several neoglycoproteins, especially  $\alpha$ -L-fucosyl-,  $\alpha$ -D-mannosyl-, N,N'-di-acetyl- $\beta$ -chitobiosyl- and  $\beta$ -D-glucosyl-BSA, were endocytosed by cultured human CD1a+ DC as well as by CD1a- CD14- cells which were also obtained in the culture. Pac-BSA and Man-BSA had the same number of binding sites (1.7 + 106/cell) on CD1a+ DC, and bound with an affinity constant close to 107 L/mol. Inhibition experiments indicated that these two neoglycoproteins bound to the same membrane lectin. CD1a+ and CD1a- cells were both labeled by an antiserum specific for the human macrophage mannose receptor. The membrane lectin specific for mannose and fucose that is evidenced in these expts. on cultured DC may be similar to the macrophage membrane lectin or may share functional and structural properties with it.

**L13 ANSWER 8 OF 11 ZCAPLUS COPYRIGHT 2007 ACS ON STN**  
**ACCESSION NUMBER:** 1994:240016 ZCAPLUS Full-text  
**DOCUMENT NUMBER:** 120:240016  
**TITLE:** Gene and protein sequence from the WO isolate of feline immunodeficiency virus and their use in diagnosis and prophylaxis of infection  
**INVENTOR(S):** Pandino, Gianfranco; Chappey, Colombe; Hurtrel, Bruno; Morallon, Anne; Klatzmann, David; Sonigo, Pierre; Saurin, William; Avrameas, Alexandre; Strohsberg, Arthur Donny  
**PATENT ASSIGNEE(S):** Centre National de la Recherche Scientifique, Fr.  
**SOURCE:** Eur. Pat. Appl., 56 pp.  
**CODEN:** EPXADM

**DOCUMENT TYPE:** Patent

**LANGUAGE:** French

**PATENT INFORMATION:** 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 577458	A1	19940105	EP 1993-401538	19930616
EP 577458	B1	20040929		
FR 2692279	A1	19931217	FR 1992-7257	19920616
FR 2692279	B1	19950519		
FR 2692269	A1	19931217	FR 1992-7258	19920616

9

**FR 2692269** B1 19950519  
**FR 2692270** A1 19931217  
**AT 278018** T 20041015  
**PRIORITY APPL. INFO.:** FR 1992-14026  
FR 1992-7257 A 19920616  
FR 1992-7258 A 19920616  
FR 1992-14026 A 19921123

**AB** Nucleotide and protein sequences from feline immunodeficiency virus (FIV) are identified and the genes used to manufacture viral peptides for use in diagnostics and prophylaxis, e.g. vaccines. Specifically, the env and gag genes and gene products are characterized as are the SU and TM epitopes of the env protein. Sequences were cloned from peripheral blood lymphocytes of infected animals by PCR using primers derived from the corresponding sequences of the Petaluma isolate. These sequences were used to construct full-length copies of the genes. Sequence divergence between the Petaluma and WO isolates were sufficient to differentiate the strains by hybridization. Immunodominant epitopes of the env protein were used in the diagnosis of infection.

**L13 ANSWER 9 OF 11 ZCAPLUS COPYRIGHT 2007 ACS ON STN**  
**ACCESSION NUMBER:** 1993:557786 ZCAPLUS Full-text  
**DOCUMENT NUMBER:** 119:157786  
**TITLE:** Serological diagnosis of feline immunodeficiency virus infection based on synthetic peptides from Env glycoproteins  
**AUTHOR(S):** Avrameas, A.; Strohsberg, A. D.; Morallon, A.; Sonigo, P.; Pandino, G.  
**CORPORATE SOURCE:** Unite Immunopharmacol. Mol. Genet. Virus, Inst. Cochin Genet. Mol., Paris, Fr.  
**SOURCE:** Research in Virology (1993), 144(3), 209-18  
**CODEN:** RESVEY; ISSN: 0923-2516

**DOCUMENT TYPE:** Journal

**LANGUAGE:** English

**AB** Feline immunodeficiency virus (FIV) is a lentivirus which infects domestic cats, causing an acquired immunodeficiency syndrome (AIDS). The aim of the present work was the development of an immunoassay for the diagnosis of FIV infection, using synthetic peptides from FIV envelope (Env) glycoproteins. Four peptides (8 to 11 amino acids long) corresponding to group-specific epitopes of FIV Env extracellular (SU) or transmembrane (TM) glycoproteins were synthesized. They were evaluated by ELISA for immunoreactivity with sera from naturally or exptl. FIV-infected cats. One of these, P237, corresponds to a conserved nonapeptide of FIV TM, folded as a loop between two cysteines. ELISA performed with P237 on 171 sera from FIV-infected cats and 46 sera from specific-pathogen-free cats showed no false pos. cases and 100% detection of infected cat sera. Thus, the P237 ELISA is a sensitive and specific immunoassay for early detection of antibodies to FIV. This synthetic nonapeptide is easier to produce and purify than virus preps. or recombinant proteins.

**L13 ANSWER 10 OF 11 ZCAPLUS COPYRIGHT 2007 ACS ON STN**  
**ACCESSION NUMBER:** 1993:37475 ZCAPLUS Full-text  
**DOCUMENT NUMBER:** 118:37475  
**TITLE:** Feline immunodeficiency virus (FIV)-derived peptide fragments, antibodies to the peptide fragments, and diagnostic and therapeutic uses thereof  
**INVENTOR(S):** Avrameas, Alexandre; Guillet, Jean Gerard; Morallon, Anne; Strohsberg, Arthur Donny  
**PATENT ASSIGNEE(S):** Centre National de la Recherche Scientifique, Fr.  
**SOURCE:** Fr. Demande, 38 pp.  
**CODEN:** FRXABL